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RAW SEQUENCE LISTING

DATE: 02/22/2002

PATENT APPLICATION: US/09/994,444

TIME: 08:55:01

Input Set : N:\Crf3\RULE60\09994444.txt

Output Set: N:\CRF3\02222002\I994444.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

(i) APPLICANT: Bates, Elizabeth E.M.
de Saint-Vis, Blandine M.
Caux, Christophe
Lebecque, Serge J.E.
Banchereau, Jacques

(ii) TITLE OF INVENTION: ISOLATED MAMMALIAN DENDRITIC CELL GENES;
RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/994,444
(B) FILING DATE: 27-Nov-2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/978,289
(B) FILING DATE: 25-NOV-1997
(A) APPLICATION NUMBER: US 60/032,767
(B) FILING DATE: 11-DEC-1996
(A) APPLICATION NUMBER: US 60/031,806
(B) FILING DATE: 27-NOV-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0669K1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196
(B) TELEFAX: (650)496-1204

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

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63      (B) TYPE: nucleic acid
64      (C) STRANDEDNESS: single
65      (D) TOPOLOGY: linear
67      (ii) MOLECULE TYPE: cDNA
70      (ix) FEATURE:
71          (A) NAME/KEY: CDS
72          (B) LOCATION: 19..513
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77  GGGCCCTTGT CTGCAGAG ATG GCT CCC AAT GCT TCC TGC CTC TGT GTG CAT      51
78                      Met Ala Pro Asn Ala Ser Cys Leu Cys Val His
79                      1          5          10
81  GTC CGT TCC GAG GAA TGG GAT TTA ATG ACC TTT GAT GCC AAC CCA TAT      99
82  Val Arg Ser Glu Glu Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr
83                      15          20          25
85  GAC AGC GTG AAA AAA ATC AAA GAA CAT GTC CGG TCT AAG ACC AAG GTT      147
86  Asp Ser Val Lys Lys Ile Lys Glu His Val Arg Ser Lys Thr Lys Val
87                      30          35          40
89  CCT GTG CAG GAC CAG GTT CTT TTG CTG GGC TCC AAG ATC TTA AAG CCA      195
90  Pro Val Gln Asp Gln Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro
91                      45          50          55
93  CGG AGA AGC CTC TCA TCT TAT GGC ATT GAC AAA GAG AAG ACC ATC CAC      243
94  Arg Arg Ser Leu Ser Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His
95  60          65          70          75
97  CTT ACC CTG AAA GTG GTG AAG CCC AGT GAT GAG GAG CTG CCC TTG TTT      291
98  Leu Thr Leu Lys Val Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe
99                      80          85          90
101 CTT GTG GAG TCA GGT GAT GAG GCA AAG AGG CAC CTC CTC CAG GTG CGA      339
102 Leu Val Glu Ser Gly Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg
103                      95          100          105
105 AGG TCC AGC TCA GTG GCA CAA GTG AAA GCA ATG ATC GAG ACT AAG ACG      387
106 Arg Ser Ser Ser Val Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr
107                      110          115          120
109 GGT ATA ATC CCT GAG ACC CAG ATT GTG ACT TGC AAT GGA AAG AGA CTG      435
110 Gly Ile Ile Pro Glu Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu
111                      125          130          135
113 GAA GAT GGG AAG ATG ATG GCA GAT TAC GGC ATC AGA AAG GGC AAC TTA      483
114 Glu Asp Gly Lys Met Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu
115 140          145          150          155
117 CTC TTC CTG GCA TCT TAT TGT ATT GGA GGG TGACCACCCT GGGGATGGGG      533
118 Leu Phe Leu Ala Ser Tyr Cys Ile Gly Gly
119                      160          165
121 TGTTGGCAGG GGTCAAAAAG CTTATTTCTT TTAATCTCTT ACTCAACGAA CACATCTTCT      593
123 GATGATTTCC CAAAATTAAT GAGAATGAGA TGAGTAGAGT AAGATTTGGG TGGGATGGGT      653
125 AGGATGAAGT ATATTGCCCA ACTCTATGTT TCTTTGATTC TAACACAATT AATTAAGTGA      713
127 CATGATTTTT ACTAATGTAT TACTGAGACT AGTAAATAAA TTTTAAAGGC AAAATAGAGC      773
129 ATTC      777
132 (2) INFORMATION FOR SEQ ID NO: 2:
134      (i) SEQUENCE CHARACTERISTICS:
135          (A) LENGTH: 165 amino acids

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136 (B) TYPE: amino acid
 137 (D) TOPOLOGY: linear
 139 (ii) MOLECULE TYPE: protein
 141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 143 Met Ala Pro Asn Ala Ser Cys Leu Cys Val His Val Arg Ser Glu Glu
 144 1 5 10 15
 146 Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys
 147 20 25 30
 149 Ile Lys Glu His Val Arg Ser Lys Thr Lys Val Pro Val Gln Asp Gln
 150 35 40 45
 152 Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser
 153 50 55 60
 155 Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His Leu Thr Leu Lys Val
 156 65 70 75 80
 158 Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Gly
 159 85 90 95
 161 Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg Arg Ser Ser Ser Val
 162 100 105 110
 164 Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu
 165 115 120 125
 167 Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu Glu Asp Gly Lys Met
 168 130 135 140
 170 Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu Leu Phe Leu Ala Ser
 171 145 150 155 160
 173 Tyr Cys Ile Gly Gly
 174 165

176 (2) INFORMATION FOR SEQ ID NO: 3:

178 (i) SEQUENCE CHARACTERISTICS:

179 (A) LENGTH: 496 base pairs

180 (B) TYPE: nucleic acid

181 (C) STRANDEDNESS: single

182 (D) TOPOLOGY: linear

184 (ii) MOLECULE TYPE: cDNA

187 (ix) FEATURE:

188 (A) NAME/KEY: CDS

189 (B) LOCATION: 8..493

192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

194 TACAGAC ATG GCT TCT GTC CGC ACC TGT GTT GTC CGT TCA GAC CAA TGG 49
 195 Met Ala Ser Val Arg Thr Cys Val Val Arg Ser Asp Gln Trp
 196 1 5 10
 198 CGG TTA ATG ACC TTT GAG ACC ACT GAG AAT GAC AAA GTG AAG AAG ATA 97
 199 Arg Leu Met Thr Phe Glu Thr Thr Glu Asn Asp Lys Val Lys Lys Ile
 200 15 20 25 30
 202 AAT GAA CAT ATT AGG TCC CAA ACC AAG GTC TCT GTA CAG GAC CAG ATC 145
 203 Asn Glu His Ile Arg Ser Gln Thr Lys Val Ser Val Gln Asp Gln Ile
 204 35 40 45
 206 CTT CTG CTA GAC TCC AAA ATC CTC AAG CCC CAT CGA AAA TTG TCA TCC 193
 207 Leu Leu Leu Asp Ser Lys Ile Leu Lys Pro His Arg Lys Leu Ser Ser
 208 50 55 60

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210 TAT GGG ATT GAC AAG GAA ACC ACT ATC CAC CTT ACC CTG AAG GTG GTG      241
211 Tyr Gly Ile Asp Lys Glu Thr Thr Ile His Leu Thr Leu Lys Val Val
212          65                      70                      75
214 AAG CCC AGT GAT GAA GAG CTG CCC TTG TTT CTG GTG GAG TCC AAA AAC      289
215 Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Lys Asn
216          80                      85                      90
218 GAG GGG CAA AGG CAC CTC CTC CGA GTT CGA AGA TCC AGC TCA GTG GCC      337
219 Glu Gly Gln Arg His Leu Leu Arg Val Arg Arg Ser Ser Ser Val Ala
220          95                      100                     105                     110
222 CAG GTG AAA GAG ATG ATC GAG AGT GTG ACC TCT GTG ATC CCT AAG AAG      385
223 Gln Val Lys Glu Met Ile Glu Ser Val Thr Ser Val Ile Pro Lys Lys
224          115                     120                     125
226 CAG GTT GTG AAT TGC AAC GGA AAG AAG CTG GAA GAT GGA AAG ATC ATG      433
227 Gln Val Val Asn Cys Asn Gly Lys Lys Leu Glu Asp Gly Lys Ile Met
228          130                     135                     140
230 GCT GAC TAC AAC ATC AAG AGT GGC AGT TTG CTC TTT CTG ACA ACA CAC      481
231 Ala Asp Tyr Asn Ile Lys Ser Gly Ser Leu Leu Phe Leu Thr Thr His
232          145                     150                     155
234 TGC ACT GGG GGA TGA      496
235 Cys Thr Gly Gly
236          160
239 (2) INFORMATION FOR SEQ ID NO: 4:
241      (i) SEQUENCE CHARACTERISTICS:
242          (A) LENGTH: 162 amino acids
243          (B) TYPE: amino acid
244          (D) TOPOLOGY: linear
246      (ii) MOLECULE TYPE: protein
248      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
250 Met Ala Ser Val Arg Thr Cys Val Val Arg Ser Asp Gln Trp Arg Leu
251      1          5          10          15
253 Met Thr Phe Glu Thr Thr Glu Asn Asp Lys Val Lys Lys Ile Asn Glu
254          20          25          30
256 His Ile Arg Ser Gln Thr Lys Val Ser Val Gln Asp Gln Ile Leu Leu
257          35          40          45
259 Leu Asp Ser Lys Ile Leu Lys Pro His Arg Lys Leu Ser Ser Tyr Gly
260          50          55          60
262 Ile Asp Lys Glu Thr Thr Ile His Leu Thr Leu Lys Val Val Lys Pro
263      65          70          75          80
265 Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Lys Asn Glu Gly
266          85          90          95
268 Gln Arg His Leu Leu Arg Val Arg Arg Ser Ser Ser Val Ala Gln Val
269          100         105         110
271 Lys Glu Met Ile Glu Ser Val Thr Ser Val Ile Pro Lys Lys Gln Val
272          115         120         125
274 Val Asn Cys Asn Gly Lys Lys Leu Glu Asp Gly Lys Ile Met Ala Asp
275          130         135         140
277 Tyr Asn Ile Lys Ser Gly Ser Leu Leu Phe Leu Thr Thr His Cys Thr
278      145         150         155         160
280 Gly Gly

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283 (2) INFORMATION FOR SEQ ID NO: 5:

285 (i) SEQUENCE CHARACTERISTICS:

286 (A) LENGTH: 1040 base pairs

287 (B) TYPE: nucleic acid

288 (C) STRANDEDNESS: single

289 (D) TOPOLOGY: linear

291 (ii) MOLECULE TYPE: cDNA

294 (ix) FEATURE:

295 (A) NAME/KEY: CDS

296 (B) LOCATION: 45..767

298 (ix) FEATURE:

299 (A) NAME/KEY: mat_peptide

300 (B) LOCATION: 111..767

303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

305	TTCCTTTCAA ATACACACCC CAACCCGCCC CGGCATACAC AGAA ATG GGG ACT GCG	56
306		Met Gly Thr Ala
307		-22 -20
309	AGC AGA AGC AAC ATC GCT CGC CAT CTG CAA ACC AAT CTC ATT CTA TTT	104
310	Ser Arg Ser Asn Ile Ala Arg His Leu Gln Thr Asn Leu Ile Leu Phe	
311		-15 -10 -5
313	TGT GTC GGT GCT GTG GGC GCC TGT ACT CTC TCT GTC ACA CAA CCG TGG	152
314	Cys Val Gly Ala Val Gly Ala Cys Thr Leu Ser Val Thr Gln Pro Trp	
315		1 5 10
317	TAC CTA GAA GTG GAC TAC ACT CAT GAG GCC GTC ACC ATA AAG TGT ACC	200
318	Tyr Leu Glu Val Asp Tyr Thr His Glu Ala Val Thr Ile Lys Cys Thr	
319	15 20 25 30	
321	TTC TCC GCA ACC GGA TGC CCT TCT GAG CAA CCA ACA TGC CTG TGG TTT	248
322	Phe Ser Ala Thr Gly Cys Pro Ser Glu Gln Pro Thr Cys Leu Trp Phe	
323		35 40 45
325	CGC TAC GGT GCT CAC CAG CCT GAG AAC CTG TGC TTG GAC GGG TGC AAA	296
326	Arg Tyr Gly Ala His Gln Pro Glu Asn Leu Cys Leu Asp Gly Cys Lys	
327		50 55 60
329	AGT GAG GCA GAC AAG TTC ACA GTG AGG GAG GCC CTC AAA GAA AAC CAA	344
330	Ser Glu Ala Asp Lys Phe Thr Val Arg Glu Ala Leu Lys Glu Asn Gln	
331		65 70 75
333	GTT TCC CTC ACT GTA AAC AGA GTG ACT TCA AAT GAC AGT GCA ATT TAC	392
334	Val Ser Leu Thr Val Asn Arg Val Thr Ser Asn Asp Ser Ala Ile Tyr	
335		80 85 90
337	ATC TGT GGA ATA GCA TTC CCC AGT GTG CCG GAA GCG AGA GCT AAA CAG	440
338	Ile Cys Gly Ile Ala Phe Pro Ser Val Pro Glu Ala Arg Ala Lys Gln	
339		95 100 105 110
341	ACA GGA GGA GGG ACC ACA CTG GTG GTA AGA GAA ATT AAG CTG CTC AGC	488
342	Thr Gly Gly Gly Thr Thr Leu Val Val Arg Glu Ile Lys Leu Leu Ser	
343		115 120 125
345	AAG GAA CTG CGG AGC TTC CTG ACA GCT CTT GTA TCA CTG CTC TCT GTC	536
346	Lys Glu Leu Arg Ser Phe Leu Thr Ala Leu Val Ser Leu Leu Ser Val	
347		130 135 140
349	TAT GTG ACC GGT GTG TGC GTG GCC TTC ATA CTC CTC TCC AAA TCA AAA	584
350	Tyr Val Thr Gly Val Cys Val Ala Phe Ile Leu Leu Ser Lys Ser Lys	

VERIFICATION SUMMARY

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DATE: 02/22/2002

TIME: 08:55:02

Input Set : N:\Crf3\RULE60\09994444.txt

Output Set: N:\CRF3\02222002\I994444.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]